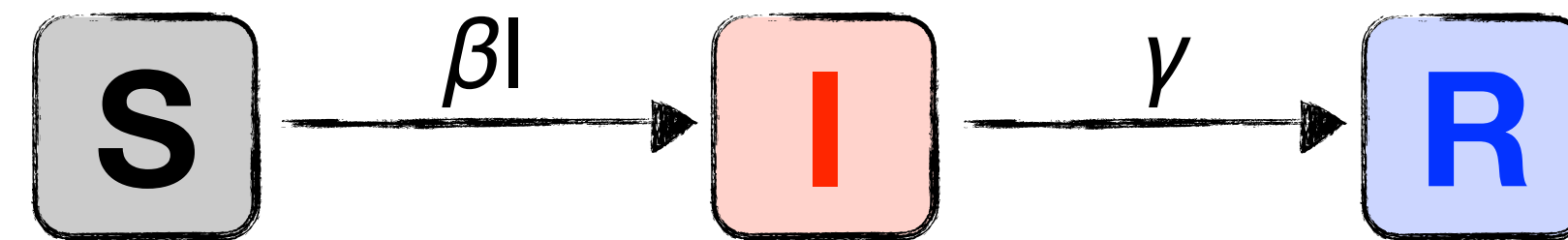


The fundamental model of disease transmission: the SIR model

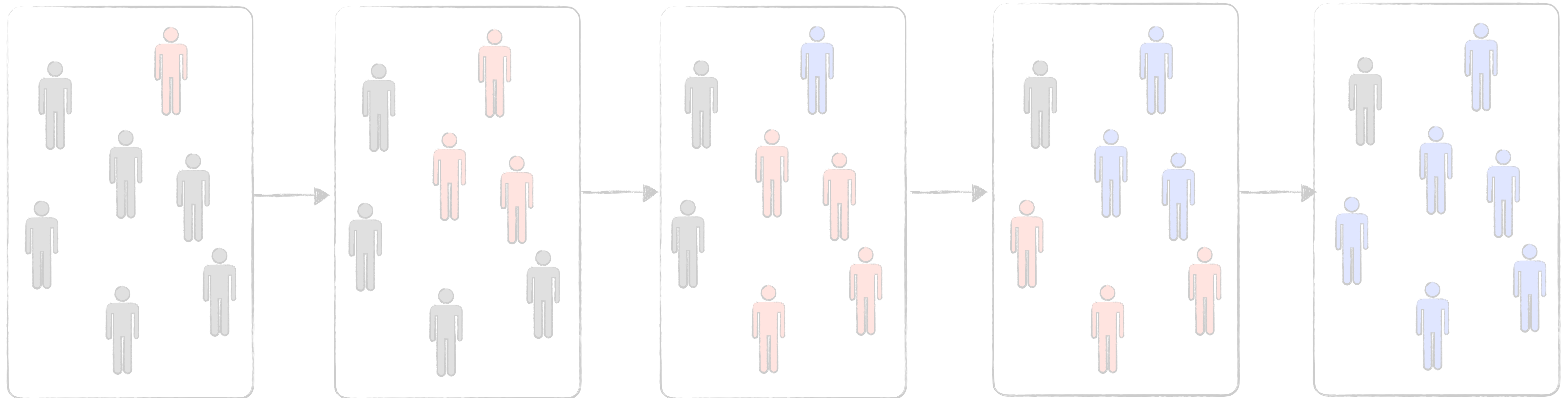
If we describe how an **individual** progresses through disease...



The **S** \rightarrow **I** transition depends on **infectiousness (β)**
and the **number of infectious people (I)**

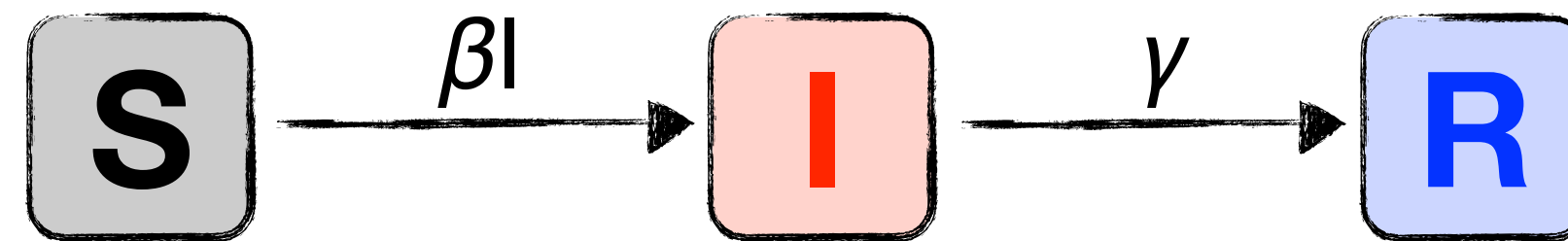
The **I** \rightarrow **R** transition depends on the **recovery rate (γ)**

Can we infer what will happen with the **population**?



The fundamental model of disease transmission: the SIR model

If we describe how an **individual** progresses through disease...



The **S** → **I** transition depends on **infectiousness** (β) and the **number of infectious people** (**I**)

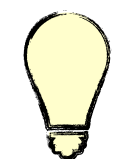
The **I** → **R** transition depends on the **recovery rate** (γ)

To translate this diagram into equations,
multiply the **rates** over the arrows by the **states** at the arrow's tail:

$$\frac{dS}{dt} = -\beta IS$$

$$\frac{dI}{dt} = \beta IS - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$



Solving these equations means asking: how do the number of people in S, I, and R vary over time, given the individual-level values we've put into the model?